

SEQUENCE LISTING

<110> Reed, Guy L.

<120> Composition and Method for Enhancing Fibrinolysis

<130> 0609.4320003

<140>

<141> 2001-10-12

<150> 08/934,000

<151> 1997-09-19

<150> 60/026,356

<151> 1996-09-20

<160> 81

<170> PatentIn version 3.1

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Alpha-2 Antiplasmin Antibody

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> May be any Amino Acid

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Xaa Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val
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Asp Ile Gln Met Thr
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<223> May be any Amino Acid

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Xaa Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val
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<222> (1)..(381)

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<222> (1)..(60)

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Met Ser Val Leu Thr Gln Val Leu Xaa Leu Leu Leu Trp Leu Thr
-20 -15 -10 -5

ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct 96
Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
1 5 10

gca tct gtg gga gaa act gtc acc atc aca tgt cga gca agt ggg aat 144
Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
15 20 25

att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct 192
Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
30 35 40

cag ctc ctg gtc tat aat gca aaa acc tta gca gat ggt gtg cca tca 240

Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
45 50 55 60

agg ttc agt ggc agt gga tca gga aca caa ttt tct ctc agg atc aac 288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Arg Ile Asn
65 70 75

agc ctg cag cct gaa gat ttt ggg agt cat tac tgt caa cat ttt tgg 336
Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
80 85 90

acc act ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa 381
Thr Thr Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
95 100 105

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<222> (9)..(9)

<223> May be either Gly or Ala

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Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
1 5 10

Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
15 20 25

Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
30 35 40

Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Arg Ile Asn
65 70 75

Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
80 85 90

Thr Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
95 100 105

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ggg gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct 96
Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
1 5 10

gca tct gtg gga gaa act gtc acc gtc aca tgt cga gca agt ggg aat 144
Ala Ser Val Gly Glu Thr Val Thr Val Thr Cys Arg Ala Ser Gly Asn

15	20	25	
att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct			192
Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro			
30	35	40	
cag ctc ctg gtc tat aat gca aga acc tta gca gat ggt gtg cca tca			240
Gln Leu Leu Val Tyr Asn Ala Arg Thr Leu Ala Asp Gly Val Pro Ser			
45	50	55	60
agg ttc agt ggc agt gga tca gga aca caa tat tct ctc aag atc aac			288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn			
65	70	75	
agc ctg cag cct gaa gat ttt ggg agt tat tac tgt caa cat ttt tgg			336
Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp			
80	85	90	
agt aat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa			381
Ser Asn Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys			
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Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser	
1	5 10

Ala Ser Val Gly Glu Thr Val Thr Val Thr Cys Arg Ala Ser Gly Asn	
15	20 25

Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro	
30	35 40

Gln Leu Leu Val Tyr Asn Ala Arg Thr Leu Ala Asp Gly Val Pro Ser	
45	50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
65 70 75

Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp
80 85 90

Ser Asn Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
95 100 105

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<222> (1)..(60)

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-20 -15 -10 -5

ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct 96
Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
1 5 10

gca tct gtg gga gaa act gtc acc atc aca tgt cga gca agt ggg aat 144
Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
15 20 25

att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct 192
Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
30 35 40

caa ctc ctg gtc tat aat gca aaa acc tta gca gat ggt gtg cca tca 240
Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
45 50 55 60

agg ttc agt ggc agt gga tca gga aca caa ttt tct ctc aag atc aac 288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn
65 70 75

agc ctg cag cct gaa gat ttt ggg agt cat tac tgt caa cat ttt tgg 336
Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
80 85 90

acc act ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa 381
Thr Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
95 100 105

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-20 -15 -10 -5

Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
1 5 10

Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
15 20 25

Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
30 35 40

Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn

65

70

75

Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
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Thr Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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-15 -10 -5

ctc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag 96
Leu Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
1 5 10

cct gga gaa aca gtc aag atc tcc tgc aag gcc tct ggg tat acc ttc 144
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25

aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta 192
 Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
 30 35 40 45

aag tgg atg ggc tgg ata aac acc aag agt gga gag cca aca tat gct 240
 Lys Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala
 50 55 60

gaa gag ttc aag gga cgg ttt gtc ttc tct ttg gaa acc tct gcc agc 288
 Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Glu Thr Ser Ala Ser
 65 70 75

act gcc cat ttg cag atc aag aat ttc aga aat gag gac acg gct aca 336
 Thr Ala His Leu Gln Ile Lys Asn Phe Arg Asn Glu Asp Thr Ala Thr
 80 85 90

tat ttc tgt gca aga tgg gta cct ggg acc tat gct atg gac tac tgg 384
 Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp
 95 100 105

ggt caa gga acc tca gtc acc gtc tcc tca 414
 Gly Gln Gly Thr Ser Val Thr Val Ser Ser
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<223> May be either Asp or Ala

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> May be either Asn or Thr

<220>

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Met Xaa Trp Val Trp Xaa Leu Leu Phe Leu Met Ala Ala Ala Gln Ser

-15

-10

-5

Leu Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
1 5 10

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25

Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
30 35 40 45

Lys Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala
50 55 60

Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Glu Thr Ser Ala Ser
65 70 75

Thr Ala His Leu Gln Ile Lys Asn Phe Arg Asn Glu Asp Thr Ala Thr
80 85 90

Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp
95 100 105

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
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-15 -10 -5	

atc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag	96
Ile Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys	
1 5 10	

cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc	144
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
15 20 25	

aca aag tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta	192
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu	
30 35 40 45	

aag tgg atg ggc tgg ata aac acc aac agt gga gag cca aca tat gct	240
Lys Trp Met Gly Trp Ile Asn Thr Asn Ser Gly Glu Pro Thr Tyr Ala	
50 55 60	

gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc	288
Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser	
65 70 75	

act gcc tat ttg cag atc aac aac ctc aaa aat gag gac tcg gct aca	336
Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Ser Ala Thr	
80 85 90	

tat ttc tgt gca aga tgg gta cct ggg acc tat gct atg gac tac tgg	384
Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp	
95 100 105	

ggt caa gga acc tca gtc acc gtc tcc tca	414
Gly Gln Gly Thr Ser Val Thr Val Ser Ser	
110 115	

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<223> May be either Asp or Ala

<220>

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<222> (6)..(6)

<223> May be either Asn or Thr

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<400> 13

Met Xaa Trp Val Trp Xaa Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
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1 5 10

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25

Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
30 35 40 45

Lys Trp Met Gly Trp Ile Asn Thr Asn Ser Gly Glu Pro Thr Tyr Ala
50 55 60

Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
65 70 75

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Ser Ala Thr
80 85 90

Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp
95 100 105

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
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-15 -10 -5	

atc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag	96
Ile Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys	
1 5 10	

cct gga gaa aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc	144
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
15 20 25	

aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta	192
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu	
30 35 40 45	

aag tgg atg ggc tgg ata aac acc aag agt gga gag cca aca tat gct	240
Lys Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala	
50 55 60	

gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc	288
Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser	
65 70 75	

act gcc aat ttg cag atc aag aac ctc aaa aat gag gac acg gct aca	336
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Thr Ala Asn Leu Gln Ile Lys Asn Leu Lys Asn Glu Asp Thr Ala Thr
80 85 90

tat ttc tgt gca aga tgg gta cct ggg acc tat gcc atg gac tac tgg 384
Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp
95 100 105

ggt caa gga acc tca gtc acc gtc tcc tca 414
Gly Gln Gly Thr Ser Val Thr Val Ser Ser
110 115

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<223> May be either Asp or Ala

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<222> (6)..(6)

<223> May be either Asn or Thr

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Ile Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
1 5 10

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25

Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
30 35 40 45

Lys Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala
50 55 60

Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
65 70 75

Thr Ala Asn Leu Gln Ile Lys Asn Leu Lys Asn Glu Asp Thr Ala Thr
80 85 90

Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp
95 100 105

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
110 115

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<212> DNA

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<221> CDS

<222> (31)..(411)

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Met Ser Val Leu Thr Gln Val Leu

-20

-15

gcg ttg ctg ctg ctg tgg ctt aca ggt gcc aga tgt gac atc cag atg	102
Ala Leu Leu Leu Leu Trp Leu Thr Gly Ala Arg Cys Asp Ile Gln Met	
-10 -5 1	
act cag tct cca tcc tcc cta tct gca tct gtg gga gac aga gtc acc	150
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr	
5 10 15 20	
atc aca tgt cga gca agt ggg aat att cac aat tat tta gca tgg tat	198
Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala Trp Tyr	
25 30 35	
cag cag aaa cag gga aaa tct cct caa ctc ctg gtc tat aat gca aaa	246
Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Asn Ala Lys	
40 45 50	
acc tta gca agt ggt gtg cca tca agg ttc agt ggc agt gga tca gga	294
Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly	
55 60 65	
aca gat ttt act ctc acc atc agc agc ctg cag cct gaa gat ttt ggg	342
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Gly	
70 75 80	
agt cat tac tgt caa cat ttt tgg acc act ccg tgg acg ttc ggt gga	390
Ser His Tyr Cys Gln His Phe Trp Thr Thr Pro Trp Thr Phe Gly Gly	
85 90 95 100	
ggc acc aag ctg gaa atc aaa	411
Gly Thr Lys Leu Glu Ile Lys	
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<223> Alpha-2 Antiplasmin Antibody

<400> 17

Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Trp Leu Thr
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Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
1 5 10

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
15 20 25

Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
30 35 40

Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Ser Gly Val Pro Ser
45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75

Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
80 85 90

Thr Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
95 100 105

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 -20 -15 -10 -5

ggg gcc aga tgt cag atc cag ttg gtg cag tct gga tct gag ctg aag 96
 Gly Ala Arg Cys Gln Ile Gln Leu Val Gln Ser Gly Ser Glu Leu Lys
 1 5 10

aag cct gga gcc tca gtc aag atc tcc tgc aag gct tct ggg tat acc 144
 Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr
 15 20 25

ttc aca aac tat gga atg aac tgg gtg cga cag gct cca gga caa ggt 192
 Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly
 30 35 40

tta gag tgg atg ggc tgg ata aac acc aag agt gga gag cca aca tat 240
 Leu Glu Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr
 45 50 55 60

gct gaa gag ttc aag gga cgg ttt gtc ttc tct ttg gac acc tct gtc 288
 Ala Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val
 65 70 75

acc act gcc tat ttg cag atc agc agc ctc aaa gct gag gac acg gct 336
 Thr Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala
 80 85 90

gtg tat ttc tgt gca aga tgg gta cct ggg acc tat gcc atg gac tac 384
 Val Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr
 95 100 105

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 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 110 115

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Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Leu Trp Leu Thr
 -20 -15 -10 -5

Gly Ala Arg Cys Gln Ile Gln Leu Val Gln Ser Gly Ser Glu Leu Lys
1 5 10

Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr
15 20 25

Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly
30 35 40

Leu Glu Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr
45 50 55 60

Ala Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val
65 70 75

Thr Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala
80 85 90

Val Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr
95 100 105

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110 115

<210> 20

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<212> DNA

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<223> Alpha-2 Antiplasmin Antibody

<220>

<221> CDS

<222> (31)..(447)

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Met Ser Val Leu Thr Gln Val Leu
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gcg ttg ctg ctg ctg tgg ctt aca ggt gcc aga tgt cag atc cag ttg 102
Ala Leu Leu Leu Leu Trp Leu Thr Gly Ala Arg Cys Gln Ile Gln Leu
-10 -5 1

gtg cag tct gga gct gag gtg aag aag cct gga gcc tca gtc aag atc 150
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Ile
5 10 15 20

tcc tgc aag gct tct ggg tat acc ttc aca aac tat gga atg aac tgg 198
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp
25 30 35

gtg cga cag gct cca gga caa ggt tta gag tgg atg ggc tgg ata aac 246
Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn
40 45 50

acc aag agt gga gag cca aca tat gct gaa gag ttc aag gga cgg ttt 294
Thr Lys Ser Gly Glu Pro Thr Tyr Ala Glu Glu Phe Lys Gly Arg Phe
55 60 65

acc ttc acc ttg gac acc tct acg agc act gcc tat ttg gag atc agg 342
Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr Leu Glu Ile Arg
70 75 80

agc ctc aga tct gac gac acg gct gtg tat ttc tgt gca aga tgg gta 390
Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys Ala Arg Trp Val
85 90 95 100

cct ggg acc tat gcc atg gac tac tgg ggt caa gga acc acg gtc acc 438
Pro Gly Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
105 110 115

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Val Ser Ser

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<400> 21

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Gly Ala Arg Cys Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys
1 5 10

Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr
15 20 25

Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly
30 35 40

Leu Glu Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr
45 50 55 60

Ala Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr
65 70 75

Ser Thr Ala Tyr Leu Glu Ile Arg Ser Leu Arg Ser Asp Asp Thr Ala
80 85 90

Val Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr
95 100 105

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
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actagtcgac atgagtgtgc tcactcaggt cctggsgett

40

<210> 25

<211> 88

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tagggagacc caagcttgg accaatTTaa attgatattc ccttaggtct cgagtctcta 60

gataaccggg caatcgattg ggattcctt 88

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gcaagaattc caatcgattg accgggta 88

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<210> 28

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41

<210> 29

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<400> 29

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32

<210> 30

<211> 24

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gagatggagt ttgg 74

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<211> 72

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attcgaagcc gg 72

<210> 33

<211> 24

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<210> 34

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24

<210> 35

<211> 21

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<400> 35

aacagctatg accatgatta c

21

<210> 36

<211> 21

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<400> 36

cacccagcct gtgcctgcct g

21

<210> 37

<211> 30

<212> DNA

<213> Artificial Sequence

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<400> 37

cgattggaat tcttgcggcc gcttgctagc

30

<210> 38

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Alpha-2 Antiplasmin Antibody

<400> 38

cttgcggccg cttgctagca tggattgggt gtggaacttg ctattcctga tggcagctgc

60

ccaaagtatc caagcacaga

80

<210> 39

<211> 80

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60

ttggatactt tgggcagctg

80

<210> 40

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<212> DNA

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aactatggaa tgaactgggt 80

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<211> 80

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tcattccata gtttgtgaag 80

<210> 42

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gacggtttgc cttctctttg 80

<210> 43

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<210> 44

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<210> 45

<211> 80

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<400> 45

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ggcataggtc ccaggtaccc 80

<210> 46

<211> 29

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<400> 46

gggaagacgg atgggccctt ggtgctagc

29

<210> 47

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Alpha-2 Antiplasmin Antibody

<400> 47

atttaaattg atatctcctt aggtctcgag

30

<210> 48

<211> 79

<212> DNA

<213> Artificial Sequence

<220>

<223> Alpha-2 Antiplasmin Antibody

<400> 48

atttaaattg atatctcctt aggtctcgag atgagtgtgc tcactcaggt cctggcggtg

60

ctgctgctgt ggcttacag

79

<210> 49

<211> 78

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ccacagcagc agcaacgc 78

<210> 50

<211> 78

<212> DNA

<213> Artificial Sequence

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<400> 50

gtctccagcc tccctatctg catctgtggg agaaactgtc accatcacat gtcgagcaag 60

tggaatatt cacaatta 78

<210> 51

<211> 78

<212> DNA

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tatagaccag gagctgagga gattttccct gtttctgctg ataccatgct aaataattgt 60

gaatattccc acttgctc 78

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ttcagtggca gtggatca 78

<210> 53

<211> 78

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ctgccactga accttgat 78

<210> 54

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cgttcggtgg aggcacca 78

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gcctccaccg aacgtccacg g 81

<210> 56

<211> 30

<212> DNA

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<212> DNA

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gcttacagggt gccagatgtc 80

<210> 58

<211> 80

<212> DNA

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ggcacctgta agccacagca 80

<210> 59

<211> 80

<212> DNA

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acaaactatg gaatgaactg 80

<210> 60

<211> 80

<212> DNA

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ttccatagtt tgtgaaggta 80

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agggacgggtt tgtcttctct 80

<210> 62

<211> 80

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<210> 63

<211> 80

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acctgggacc tatgccatgg 80

<210> 64

<211> 80

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ataggtccca ggtacccatc 80

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agaagcctgg agcctcagtc 80

<210> 66

<211> 80

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agggacggtt taccttcacc 80

<210> 67

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gtaaaccgtc ccttgaactc 80

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acctgggacc tatgcatgg 80

<210> 69

<211> 78

<212> DNA

<213> Artificial Sequence

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<223> Alpha-2 Antiplasmin Antibody

<400> 69

agatgcagat agggaggatg gagactgagt catctggatg tcacatctgg cacctgtaag 60

ccacagcagc agcaacgc 78

<210> 70

<211> 78

<212> DNA

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<223> Alpha-2 Antiplasmin Antibody

<400> 70

gtctccatcc tccctatctg catctgtggg agacagagtc accatcacat gtcgagcaag 60

tgggaatatt cacaatta 78

<210> 71

<211> 78

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<400> 71

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ttcagtgga gtggatca 78

<210> 72

<211> 78

<212> DNA

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ctgccactga accttgat 78

<210> 73

<211> 18

<212> PRT

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<400> 73

Tyr Pro Arg Ser Ile Tyr Ile Arg Arg Arg His Pro Ser Pro Ser Leu
1 5 10 15

Thr Thr

<210> 74

<211> 15

<212> PRT

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<400> 74

Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser
1 5 10 15

<210> 75

<211> 107

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<223> May be any Amino Acid

<400> 75

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Glu Thr Val Thr Xaa Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Xaa Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Xaa Ser Leu Xaa Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Ser Xaa Tyr Cys Gln His Phe Trp Xaa Xaa Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 76

<211> 107

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<222> (74)..(74)

<223> May be any Amino Acid

<400> 76

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1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Xaa Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp Thr Thr Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 77

<211> 107

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<223> May be any Amino Acid

<400> 77

Asp Ile Gln Met Thr Gln Ser Pro Xaa Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Xaa Xaa Val Thr Xaa Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Xaa Thr Leu Ala Xaa Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Xaa Xaa Xaa Leu Xaa Ile Xaa Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Ser Xaa Tyr Cys Gln His Phe Trp Xaa Xaa Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 78

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<223> May be any Amino Acid

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<222> (89)..(89)

<223> May be any Amino Acid

<400> 78

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Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Xaa Phe Xaa Leu Asp Thr Ser Xaa Ser Thr Ala Tyr
65 70 75 80

Leu Xaa Ile Xaa Ser Leu Xaa Xaa Xaa Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 79

<211> 119

<212> PRT

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20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Xaa Ser Gly Glu Pro Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Xaa Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Xaa
65 70 75 80

Leu Gln Ile Xaa Asn Xaa Xaa Asn Glu Asp Xaa Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser
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			20					25					30		

Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Lys	Trp	Met
		35					40					45			

Gly	Trp	Ile	Asn	Thr	Lys	Ser	Gly	Glu	Pro	Thr	Tyr	Ala	Glu	Glu	Phe
	50					55					60				

Lys Gly Arg Phe Xaa Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Xaa
65 70 75 80

Leu Gln Ile Lys Asn Xaa Xaa Asn Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser
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Xaa Val Lys Ile Ser Cys Xaa Ala Ser Gly Tyr Thr Phe Thr Xaa Tyr
20 25 30

Gly Met Asn Trp Val Xaa Gln Ala Pro Gly Xaa Gly Leu Xaa Trp Met
35 40 45

Gly Trp Ile Asn Thr Xaa Ser Gly Glu Pro Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Xaa Phe Xaa Leu Xaa Thr Ser Xaa Ser Thr Ala Xaa
65 70 75 80

Leu Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Ala Xaa Tyr Phe Cys
85 90 95

Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Xaa Val Thr Val Ser Ser
115